Zheng-Zheng (Jane) Tang

CONTACT INFORMATION

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RESEARCH INTERESTS

Statistical Genetics, Genetic Epidemiology, Semiparametric Inference, Measurement Error, Bioinformatics, Survival Analysis

EDUCATION

University of North Carolina at Chapel Hill, Chapel Hill, NC

Ph.D., Biostatistics, August 2014

Advisor: Danyu Lin, Dennis Gillings Distinguished Professor

M.S., Biostatistics, May 2009

Wuhan University, Wuhan, China

B.S., Mathematics, June 2007

B.S., Biology, June 2007

PROFESSIONAL EXPERIENCE

Graduate Research Assistant, September 2010 - Present
Department of Biostatistics, UNC-CH
Supervisor: Dr. Danyu Lin

- Developed methods for gene-based association analysis of rare variants in sequencing studies for various study designs and phenotypes.
- Developed meta-analysis methods for sequenced studies.
- Developed software SCORE-Seq, SCORE-SeqTDS and MASS.
- Participated in National Heart, Lung, and Blood Institute-Exome Sequencing Project (NHLBI ESP) and collaborated with multiple phenotype analysis groups to develop the QC and analysis pipeline for the sequencing data from NHLBI ESP.

Summer Internship, June 2010 - September 2010
GlaxoSimithKline (GSK), Department of Quantitative Sciences
Supervisor: Dr. Matthew R. Nelson

- Participated in the GSK deep-sequencing project to characterize drug target genes and to identify potential drug repositioning opportunities. Developed methods for estimating sequencing error rate based on sample duplicates, parent-child trios and unrelated samples.

Graduate Research Assistant, September 2008 - June 2010
Collaborative Studies Coordinating Center, UNC-CH
Supervisor: Dr. Lloyd Chambless

- Data management from Atherosclerosis Risk In Communities (ARIC) Study. Analyzed association between novel biomarkers and various clinical cardiovascular diseases in ARIC study. Involved in preparation of manuscripts.

Graduate Research Assistant, June 2008 - September 2008
Department of Biostatistics, UNC-CH
Supervisor: Dr. Wei Sun and Dr. Fred Wright

- An analysis of the high-density single nucleotide polymorphism (SNP) arrays data for the detection of copy number variation (CNV). Developed the R package "genoCN".

Graduate Research Assistant, September 2007 - June 2008
School of Nursing, UNC-CH
Supervisor: Dr. Jill Hamilton
- Data management and statistical analysis for the project investigating the quality of life of African American cancer survivors.

Teaching Assistant
Department of Biostatistics, UNC-CH
- *BIOS 735: Statistical Computing-Basic Principles and Applications*, Fall 2013
  - Advanced course for biostatistics Ph.D. students.
- *BIOS 545: Principles of Experimental Analysis*, Spring 2010
  - Introductory biostatistics course for non-biostatistics students.

Honors & Awards

- ASA Biometrics Section Student Travel Award, 2014
- NIH Travel Award, Advanced Gene Mapping Course, 2013
- Sandra Winn Green Scholarship, School of Public Health, UNC-CH, 2012
- GSK Workshop Funds, 2012
- Student Travel Award, Biostatistics, UNC-CH, 2011, 2013
- Special Commendation for Highest Score in Qualifying Exam, Biostatistics, UNC-CH, 2009
- Regina C. Elandt-Johnson Master's Paper Award, Biostatistics, UNC-CH, 2010
- Honorable Mention for Mathematical Contest in Modeling in USA, 2007
- Outstanding Undergraduate Student Paper for Mathematics Bachelor Degree, China, 2007
- Outstanding Student Award, Wuhan University, China, 2003-2006

Professional Services

Reviewer for Genetic Epidemiology, PLOS ONE, Statistical Methods in Medical Research, Acta Biotheoretica, BMC Genetics
Wiley Science Advisor

Publications

Published:

1. **Tang ZZ**, Lin DY (2014). "Meta-analysis of sequencing studies with heterogeneous genetic associations", ***Genetic Epidemiology***.

2. Crosby J, Peloso GM, Auer PL, Crosslin D, Stitziel NO, Lange LA, Lu K, **Tang ZZ**, ..., Reiner AP, Boerwinkle E, Kathiresan S (2014). "Rare loss-of-function mutations in the APOC3 gene, plasma triglycerides, and risk for coronary heart disease", ***New England Journal of Medicine***, accepted.

3. Lange LA, Hu Y, Zhang H, Xue C, Schmidt EM, **Tang ZZ**, ..., Willer CJ (2014). "Novel rare and low frequency coding variants associated with LDL cholesterol", ***American Journal of Human Genetics***, 94, 233–245.

4. **Tang ZZ**, Lin DY (2013). "MASS: meta-analysis of score statistics for sequencing studies", ***Bioinformatics***, 29, 1803-1805.

5. Lin DY, Zeng D, **Tang ZZ** (2013). "Quantitative trait analysis in sequencing studies under trait-dependent sampling", ***Proceedings of the National Academy of Sciences of the United States of America***, 110, 12247-12252.

6. Nelson MR, Wegmann D, Ehm MG, Kessner D, Jean PS, Verzilli C, Shen J, **Tang Z**, ..., Novembre J, Mooser V (2012). "An abundance of rare functional variants in 202 drug target genes sequenced in 14,002 people", ***Science***, 337, 100–104.

7. Yang EY, Chambless L, Sharrett AR, Virani SS, Liu X, **Tang Z**, Boerwinkle E, Ballantyne CM, Nambi V (2012). "Carotid arterial wall characteristics are associated with incident ischemic stroke but not coronary heart disease in the Atherosclerosis Risk in Communities (ARIC) study", ***Stroke***, 43, 103-108.

8. Lin DY, **Tang ZZ** (2011). "A general framework for detecting disease associations with rare variants in sequencing studies", ***The American Journal of Human Genetics***, 89, 354-367.

9. Yang EY, Nambi V, **Tang Z**, Virani SS, Boerwinkle E, Hoogeveen RC, Astor BC, Mosley TH, Coresh J, Chambless L, Ballantyne CM (2009). "Clinical implications of JUPITER (Justification for the Use of statins in Prevention: an Intervention Trial Evaluating Rosuvastatin) in a U.S. population insights from the ARIC (Atherosclerosis Risk in Communities) study", ***Journal of the American College of Cardiology***, 54, 2388-2395.

10. Sun W, Wright FA, **Tang Z**, Nordgard SH, Van Loo P, Yu T, Kristensen VN, Perou CM (2009). "Integrated study of copy number states and genotype calls using high-density SNP arrays", ***Nucleic Acids Research***, 37, 5365-5377.

Talks & Posters

Invited seminar talk, "A general framework for meta-analysis of sequencing studies", Department of Biostatistics, the Vanderbilt University, Nashville, TN. (April 2014).

Invited seminar talk, "A general framework for meta-analysis of sequencing studies", Department of Biostatistics, the University of Michigan, Ann Arbor, MI. (March 2014).

Contributed talk, "Meta-analysis of sequencing studies under random-effects models", ENAR, Baltimore, MD. (March 2014).

Invited seminar talk, "A general framework for meta-analysis of sequencing studies", Department of Statistics, the University of Missouri, Columbia, MO. (February 2014).

Invited seminar talk, "A general framework for meta-analysis of sequencing studies", Department of Mathematical Sciences, the Worcester Polytechnic Institute, Worcester, MA. (January 2014).

Contributed poster, "Meta-analysis of sequencing studies under random-effects models", ASHG, Boston, MA. (October 2013).

Contributed poster, "Binary trait analysis in sequencing studies under trait-dependent sampling", IGES, Chicago, IL. (September 2013).

Contributed talk, "Binary trait analysis in sequencing studies under trait-dependent sampling", JSM, Montreal, Canada. (August 2013).

Contributed talk, "Estimating and improving next-generation sequence-based genotype accuracy", ENAR, Miami, FL. (March 2011).

Software Developed

SCORE-Seq

A C program which implements score statistics for detecting disease associations with rare variants in sequencing studies.
http://dlin.web.unc.edu/software/score-seq/

SCORE-SeqTDS

A C program for analyzing primary and secondary traits in sequencing studies under trait-dependent sampling.
http://dlin.web.unc.edu/software/score-seqtds/

MASS

A C program for the meta-analysis of sequencing studies.
http://dlin.web.unc.edu/software/mass/

genoCN

An R package for identifying copy number states and genotype calls using the SNP arrays data.
http://www.bios.unc.edu/ weisun/software/genoCN.htm

COMPUTATIONAL SKILLS

- Programming Languages: proficient in C, knowledgeable in PYTHON
- Software: proficient in R and SAS, knowledgeable in MATLAB
- Operating Systems: Unix and Windows

PROFESSIONAL MEMBERSHIPS

- Eastern North American Region/International Biometric Society
- American Statistical Association
- International Genetic Epidemiology Society
- American Society of Human Genetics